

## SEQUENCE LISTING

<110> H. William Harris  
Edward M. Brown  
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<120> Polycation-Sensing Receptor in Aquatic  
Species and Methods of Use Thereof

<130> 2856.1001-007

<140> 09/162,021

<141> 1998-09-28

<150> PCT/US97/05031

<151> 1997-03-27

<150> 08/622,738

<151> 1996-03-27

<160> 19

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 Lys Arg Asp Ile Cys Ile Asp Phe Ser Glu Met Ile Ser Gln Tyr Tyr  
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His Val Val Gly Gly Thr Ile Gly Phe Ala Leu Arg Ala Gly Arg Ile	
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Pro Gly Phe Asn Lys Phe Leu Lys Glu Val His Pro Ser Arg Ser Ser	
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Arg Thr Ala Leu Arg His Pro Cys Thr Gly Glu Glu Asn Ile Thr Ser	
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Val	Glu	Val	Ile	Ala	Ile	Leu	Ala	Ser	Ser	Phe	Gly	Leu	Leu	Gly	Cys		
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Ile	Tyr	Phe	Asn	Lys	Cys	Tyr	Ile	Ile	Leu	Phe	Lys	Pro	Cys	Arg	Asn		
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100495-100496

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Arg Pro Thr Thr Met Glu Glu Thr \*  
1020 1025

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Lys Gly Asp Ile Ile Leu Gly Gly Leu Phe Pro Ile His Phe Gly Val  
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65 70 75 80  
Ala Ile Glu Glu Ile Asn Asn Ser Met Thr Phe Leu Pro Asn Ile Thr  
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Leu Gly Tyr Arg Ile Phe Asp Thr Cys Asn Thr Val Ser Lys Ala Leu  
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Glu Ala Thr Leu Ser Phe Val Ala Gln Asn Lys Ile Asp Ser Leu Asn  
115 120 125  
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130 135 140  
Val Val Gly Ala Thr Gly Ser Gly Ile Ser Thr Ala Val Ala Asn Leu  
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Leu Gly Leu Phe Tyr Ile Pro Gln Val Ser Tyr Ala Ser Ser Ser Arg  
165 170 175  
Leu Leu Ser Asn Lys Asn Glu Tyr Lys Ala Phe Leu Arg Thr Ile Pro  
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Gln Trp Asn Trp Val Gly Thr Leu Ala Ala Asp Asp Tyr Gly Arg  
210 215 220  
Pro Gly Ile Asp Lys Phe Arg Glu Glu Ala Val Lys Arg Asp Ile Cys  
225 230 235 240  
Ile Asp Phe Ser Glu Met Ile Ser Gln Tyr Tyr Thr Gln Lys Gln Leu  
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10015456121001

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Ser	Ser	Ser	Leu	Ile	Ala	Lys	Pro	Glu	Tyr	Phe	His	Val	Val	Gly	Gly
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Gln	Gly	Asp	Gly	Ser	Lys	Ala	Gly	Asn	Ser	Arg	Arg	Thr	Ala	Leu	Arg
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Met	Gly	Glu	Gln	Val	Asp	Phe	Asp	Asp	Gln	Gly	Asp	Leu	Lys	Gly	Asn
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Val	Phe	Ile	Lys	Phe	Arg	Asn	Thr	Pro	Ile	Val	Lys	Ala	Thr	Asn	Arg
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Ser	Leu	His	Arg	Lys	Trp	Val	Gly	Leu	Asn	Leu	Gln	Phe	Leu	Leu	Val
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Phe Ser Met Leu Ile Phe Phe Ile Val Trp Ile Ser Phe Ile Pro Ala
      820      825      830
Tyr Val Ser Thr Tyr Gly Lys Phe Val Ser Ala Val Glu Val Ile Ala
      835      840      845
Ile Leu Ala Ser Ser Phe Gly Leu Leu Gly Cys Ile Tyr Phe Asn Lys
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Cys Tyr Ile Ile Leu Phe Lys Pro Cys Arg Asn Thr Ile Glu Glu Val
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945      950      955      960
Leu Ser Arg Thr Ala Arg Ser Arg Asn Ser Ala Asp Gly Arg Ser Gly
      965      970      975
Asp Asp Leu Pro Ser Arg His His Asp Gln Gly Pro Pro Gln Lys Cys
      980      985      990
Glu Pro Gln Pro Ala Asn Asp Ala Arg Tyr Lys Ala Ala Pro Thr Lys
      995      1000      1005
Gly Thr Leu Glu Ser Pro Gly Gly Ser Lys Glu Arg Pro Thr Thr Met
1010      1015      1020
Glu Glu Thr
1025

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<210> 3  
 <211> 784  
 <212> DNA  
 <213> squalus acanthias

<220>  
 <221> CDS  
 <222> (1)...(784)

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<400> 3
cta cta gtc ata tgg att gcg gcg gay gay gat tat ggc cgc cca ggg   48
Leu Leu Val Ile Trp Ile Ala Ala Asp Asp Asp Tyr Gly Arg Pro Gly
  1             5             10             15

ata gat aag ttt cga gaa gaa gct gaa gag agg gac atc tgc ata gat   96
Ile Asp Lys Phe Arg Glu Glu Ala Glu Glu Arg Asp Ile Cys Ile Asp
      20             25             30

ttc aat gag atg att tct cag tac tat aca caa aaa gag ctg gag ttt   144
Phe Asn Glu Met Ile Ser Gln Tyr Tyr Thr Gln Lys Glu Leu Glu Phe

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35	40	45	
att gca gat act att cag aat tcc tca gcc aaa gtg att gty gtc ttc Ile Ala Asp Thr Ile Gln Asn Ser Ser Ala Lys Val Ile Xaa Val Phe 50 55 60			192
tca aat ggc cct gac ttg gaa cca cta ata caa gag ata gtt cga cgg Ser Asn Gly Pro Asp Leu Glu Pro Leu Ile Gln Glu Ile Val Arg Arg 65 70 75 80			240
aac ata act gat aga ata tgg cta gca agt gaa gcg tgg gct agt tcc Asn Ile Thr Asp Arg Ile Trp Leu Ala Ser Glu Ala Trp Ala Ser Ser 85 90 95			288
tca ctg ata gcc aaa cca gaa tac ttc cat gtt gtt ggt gga acc att Ser Leu Ile Ala Lys Pro Glu Tyr Phe His Val Val Gly Gly Thr Ile 100 105 110			336
gga ttt gca cta aga gca gga cgc atc cca gga ttc cat gag ttt tta Gly Phe Ala Leu Arg Ala Gly Arg Ile Pro Gly Phe His Glu Phe Leu 115 120 125			384
aaa aag gtc cat ccc agc agg tcc tcc cac aat ggc ttt gtc aag gaa Lys Lys Val His Pro Ser Arg Ser Ser His Asn Gly Phe Val Lys Glu 130 135 140			432
ttc tgg gaa gaa aca ttt aat tgt tat ttc act gaa gaa tcc cta aca Phe Trp Glu Glu Thr Phe Asn Cys Tyr Phe Thr Glu Glu Ser Leu Thr 145 150 155 160			480
caa cta aag aat tgc aaa aca cca acc cat gga tta gca atg cac aat Gln Leu Lys Asn Cys Lys Thr Pro Thr His Gly Leu Ala Met His Asn 165 170 175			528
gac agt gcg aaa atg ggg cat tcc aca agg aca acg tta cga cct cca Asp Ser Ala Lys Met Gly His Ser Thr Arg Thr Thr Leu Arg Pro Pro 180 185 190			576
tgc act gga gaa gag aat atc acg agt gtg gag acc cct tac ctg gat Cys Thr Gly Glu Glu Asn Ile Thr Ser Val Glu Thr Pro Tyr Leu Asp 195 200 205			624
tat act cac ctg cgt att tca tat aat gtg tat gtg gca gtg tat tgg Tyr Thr His Leu Arg Ile Ser Tyr Asn Val Tyr Val Ala Val Tyr Ser 210 215 220			672
att gct cac gct ctg cag gac atc tat gcc tgc aca cct ggg aag ggg Ile Ala His Ala Leu Gln Asp Ile Tyr Ala Cys Thr Pro Gly Lys Gly 225 230 235 240			720
att ttt gcg aac gga tca tgt gcc gat atc aaa aaa gtc gaa gcc tgg Ile Phe Ala Asn Gly Ser Cys Ala Asp Ile Lys Lys Val Glu Ala Trp 245 250 255			768
aat cca tat gac tag t Asn Pro Tyr Asp *			784
260			

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<210> 4  
<211> 260  
<212> PRT  
<213> squalus acanthias

<400> 4  
Leu Leu Val Ile Trp Ile Ala Ala Asp Asp Asp Tyr Gly Arg Pro Gly  
1 5 10 15  
Ile Asp Lys Phe Arg Glu Glu Ala Glu Glu Arg Asp Ile Cys Ile Asp  
20 25 30  
Phe Asn Glu Met Ile Ser Gln Tyr Tyr Thr Gln Lys Glu Leu Glu Phe  
35 40 45  
Ile Ala Asp Thr Ile Gln Asn Ser Ser Ala Lys Val Ile Val Val Phe  
50 55 60  
Ser Asn Gly Pro Asp Leu Glu Pro Leu Ile Gln Glu Ile Val Arg Arg  
65 70 75 80  
Asn Ile Thr Asp Arg Ile Trp Leu Ala Ser Glu Ala Trp Ala Ser Ser  
85 90 95  
Ser Leu Ile Ala Lys Pro Glu Tyr Phe His Val Val Gly Gly Thr Ile  
100 105 110  
Gly Phe Ala Leu Arg Ala Gly Arg Ile Pro Gly Phe His Glu Phe Leu  
115 120 125  
Lys Lys Val His Pro Ser Arg Ser Ser His Asn Gly Phe Val Lys Glu  
130 135 140  
Phe Trp Glu Glu Thr Phe Asn Cys Tyr Phe Thr Glu Glu Ser Leu Thr  
145 150 155 160  
Gln Leu Lys Asn Cys Lys Thr Pro Thr His Gly Leu Ala Met His Asn  
165 170 175  
Asp Ser Ala Lys Met Gly His Ser Thr Arg Thr Thr Leu Arg Pro Pro  
180 185 190  
Cys Thr Gly Glu Glu Asn Ile Thr Ser Val Glu Thr Pro Tyr Leu Asp  
195 200 205  
Tyr Thr His Leu Arg Ile Ser Tyr Asn Val Tyr Val Ala Val Tyr Ser  
210 215 220  
Ile Ala His Ala Leu Gln Asp Ile Tyr Ala Cys Thr Pro Gly Lys Gly  
225 230 235 240  
Ile Phe Ala Asn Gly Ser Cys Ala Asp Ile Lys Lys Val Glu Ala Trp  
245 250 255  
Asn Pro Tyr Asp  
260

<210> 5  
<211> 598  
<212> DNA  
<213> squalus acanthias

<220>  
<221> CDS  
<222> (3)...(598)

<400> 5  
tt ctg aca ata ttt gct gtg cta gga ata ctg atc act tcc ttt gtt 47  
Leu Thr Ile Phe Ala Val Leu Gly Ile Leu Ile Thr Ser Phe Val  
1 5 10 15  
ttg gga gta ttc att aag ttc aga aat act cct att gtg aaa gcc act 95  
Leu Gly Val Phe Ile Lys Phe Arg Asn Thr Pro Ile Val Lys Ala Thr  
20 25 30

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aac aga gaa ctc tcc tat ctc ctc ctc ttc tcc tta atc tgc tgt ttc 143
Asn Arg Glu Leu Ser Tyr Leu Leu Leu Phe Ser Leu Ile Cys Cys Phe
      35              40              45

tcc agc tca ttg atc ttc att gga gaa ccc aaa gat tgg acc tgc aga 191
Ser Ser Ser Leu Ile Phe Ile Gly Glu Pro Lys Asp Trp Thr Cys Arg
      50              55              60

ctg cgt caa cct gca ttt gga atc agc ttt gtg ctg tgc att tct tgc 239
Leu Arg Gln Pro Ala Phe Gly Ile Ser Phe Val Leu Cys Ile Ser Cys
      65              70              75

att ctg gtg aaa act aat cgt gtg cta ttg gtc ttt gag gcc aag atc 287
Ile Leu Val Lys Thr Asn Arg Val Leu Leu Val Phe Glu Ala Lys Ile
      80              85              90              95

cca act agc ctc cat cga aag tgg gtg ggc ctc aat ttg caa ttc tta 335
Pro Thr Ser Leu His Arg Lys Trp Val Gly Leu Asn Leu Gln Phe Leu
      100              105              110

ctg gtt ttc ctc tgt att ctt gtg caa att gtt act tgt gtc atc tgg 383
Leu Val Phe Leu Cys Ile Leu Val Gln Ile Val Thr Cys Val Ile Trp
      115              120              125

ctt tac aca gca ccc cct tcg agc tac aga aat cat gaa cta gaa gat 431
Leu Tyr Thr Ala Pro Pro Ser Ser Tyr Arg Asn His Glu Leu Glu Asp
      130              135              140

gaa atc att ttt att aca tgt gat gaa ggt tcc tta atg gca ctt ggt 479
Glu Ile Ile Phe Ile Thr Cys Asp Glu Gly Ser Leu Met Ala Leu Gly
      145              150              155

ttt ctc att ggt tac aca tgc ctc ctt gct gcc att tgc ttc ttt ttt 527
Phe Leu Ile Gly Tyr Thr Cys Leu Leu Ala Ala Ile Cys Phe Phe Phe
      160              165              170              175

gcc ttt aag tct cgc aaa ctc cca gag aac ttc aat gag gcc aaa ttt 575
Ala Phe Lys Ser Arg Lys Leu Pro Glu Asn Phe Asn Glu Ala Lys Phe
      180              185              190

att acc ttc agc atg ctg ata tt 598
Ile Thr Phe Ser Met Leu Ile
      195

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<210> 6

<211> 198

<212> PRT

<213> squalus acanthias

<400> 6

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Leu Thr Ile Phe Ala Val Leu Gly Ile Leu Ile Thr Ser Phe Val Leu
 1          5          10          15
Gly Val Phe Ile Lys Phe Arg Asn Thr Pro Ile Val Lys Ala Thr Asn
      20          25          30
Arg Glu Leu Ser Tyr Leu Leu Leu Phe Ser Leu Ile Cys Cys Phe Ser
      35          40          45
Ser Ser Leu Ile Phe Ile Gly Glu Pro Lys Asp Trp Thr Cys Arg Leu

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50 55 60  
 Arg Gln Pro Ala Phe Gly Ile Ser Phe Val Leu Cys Ile Ser Cys Ile  
 65 70 75 80  
 Leu Val Lys Thr Asn Arg Val Leu Leu Val Phe Glu Ala Lys Ile Pro  
 85 90 95  
 Thr Ser Leu His Arg Lys Trp Val Gly Leu Asn Leu Gln Phe Leu Leu  
 100 105 110  
 Val Phe Leu Cys Ile Leu Val Gln Ile Val Thr Cys Val Ile Trp Leu  
 115 120 125  
 Tyr Thr Ala Pro Pro Ser Ser Tyr Arg Asn His Glu Leu Glu Asp Glu  
 130 135 140  
 Ile Ile Phe Ile Thr Cys Asp Glu Gly Ser Leu Met Ala Leu Gly Phe  
 145 150 155 160  
 Leu Ile Gly Tyr Thr Cys Leu Leu Ala Ala Ile Cys Phe Phe Phe Ala  
 165 170 175  
 Phe Lys Ser Arg Lys Leu Pro Glu Asn Phe Asn Glu Ala Lys Phe Ile  
 180 185 190  
 Thr Phe Ser Met Leu Ile  
 195

<210> 7  
 <211> 594  
 <212> DNA  
 <213> psuedupleuronecies americanus

<220>  
 <221> CDS  
 <222> (2)...(592)

<400> 7  
 g ttg acc ata tgt gca gtg ctg ggt gtt gcc ytg acg ggc ttc gtg atg 49  
 Leu Thr Ile Cys Ala Val Leu Gly Val Ala Xaa Thr Gly Phe Val Met  
 1 5 10 15

gcc gtc ttt gtc cga ttc cgc aac acc cca ata gtg aaa gcc acg aac 97  
 Ala Val Phe Val Arg Phe Arg Asn Thr Pro Ile Val Lys Ala Thr Asn  
 20 25 30

cga gaa ctg tcc tac gtc ctc ctg ttc tct ctc atc tgt tgc ttc tcc 145  
 Arg Glu Leu Ser Tyr Val Leu Leu Phe Ser Leu Ile Cys Cys Phe Ser  
 35 40 45

agc tcc ctc atc ttc ata gga gag ccg cag gat tgg atg tgc cgc tta 193  
 Ser Ser Leu Ile Phe Ile Gly Glu Pro Gln Asp Trp Met Cys Arg Leu  
 50 55 60

cgc caa ccg gcc ttt ggg atc agt ttt gtt ctc tgt atc tcg tgc atc 241  
 Arg Gln Pro Ala Phe Gly Ile Ser Phe Val Leu Cys Ile Ser Cys Ile  
 65 70 75 80

ctt gtg aaa aca aac cka gtc ctc ttg gtg ttt gaa gcc aag atc ccg 289  
 Leu Val Lys Thr Asn Xaa Val Leu Leu Val Phe Glu Ala Lys Ile Pro  
 85 90 95

aca agt ctc cat cgt aaa tgg tgg ggg tta aac cta cag ttc ctg ctg 337  
 Thr Ser Leu His Arg Lys Trp Trp Gly Leu Asn Leu Gln Phe Leu Leu  
 100 105 110

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gtg ttt ctg tgc aca ttt gtc caa gtc atg ata tgt gtg gtc tgg ctg 385
Val Phe Leu Cys Thr Phe Val Gln Val Met Ile Cys Val Val Trp Leu
      115      120      125

tac aac gcc cca cct tcc agt tac agg aat tat gac ata gat gag atg 433
Tyr Asn Ala Pro Pro Ser Ser Tyr Arg Asn Tyr Asp Ile Asp Glu Met
      130      135      140

att ttt atc aca tgt aat gaa ggc tct gta atg gct ctt ggg ttt ctt 481
Ile Phe Ile Thr Cys Asn Glu Gly Ser Val Met Ala Leu Gly Phe Leu
145      150      155      160

att ggc tat aca tgc ctg ctg gcc gct ata tgt ttc ttc ttt gca ttc 529
Ile Gly Tyr Thr Cys Leu Leu Ala Ala Ile Cys Phe Phe Phe Ala Phe
      165      170      175

aaa tca cgg aaa ctt cca gaa aac ttc acc gag gct aag ttc atc act 577
Lys Ser Arg Lys Leu Pro Glu Asn Phe Thr Glu Ala Lys Phe Ile Thr
      180      185      190

ttt agt atg ctc ata tt 594
Phe Ser Met Leu Ile
      195

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<210> 8  
 <211> 197  
 <212> PRT  
 <213> psuedupleuronecies americanus

<220>  
 <221> VARIANT  
 <222> (1)...(197)  
 <223> Xaa = Any Amino Acid

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<400> 8
Leu Thr Ile Cys Ala Val Leu Gly Val Ala Leu Thr Gly Phe Val Met
1      5      10      15
Ala Val Phe Val Arg Phe Arg Asn Thr Pro Ile Val Lys Ala Thr Asn
20      25      30
Arg Glu Leu Ser Tyr Val Leu Leu Phe Ser Leu Ile Cys Cys Phe Ser
35      40      45
Ser Ser Leu Ile Phe Ile Gly Glu Pro Gln Asp Trp Met Cys Arg Leu
50      55      60
Arg Gln Pro Ala Phe Gly Ile Ser Phe Val Leu Cys Ile Ser Cys Ile
65      70      75      80
Leu Val Lys Thr Asn Xaa Val Leu Leu Val Phe Glu Ala Lys Ile Pro
85      90      95
Thr Ser Leu His Arg Lys Trp Trp Gly Leu Asn Leu Gln Phe Leu Leu
100      105      110
Val Phe Leu Cys Thr Phe Val Gln Val Met Ile Cys Val Val Trp Leu
115      120      125
Tyr Asn Ala Pro Pro Ser Ser Tyr Arg Asn Tyr Asp Ile Asp Glu Met
130      135      140
Ile Phe Ile Thr Cys Asn Glu Gly Ser Val Met Ala Leu Gly Phe Leu
145      150      155      160
Ile Gly Tyr Thr Cys Leu Leu Ala Ala Ile Cys Phe Phe Phe Ala Phe
165      170      175
Lys Ser Arg Lys Leu Pro Glu Asn Phe Thr Glu Ala Lys Phe Ile Thr

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10016495 "1200T" 9649T001

180  
Phe Ser Met Leu Ile  
195

185

190

<210> 9  
<211> 475  
<212> DNA  
<213> paralichthus dentalus

<220>  
<221> CDS  
<222> (3)...(473)

<400> 9  
tg tcg tgg acg gag ccc ttt ggg atc gcg ttg gcc ata tgt gca gcg 47  
Ser Trp Thr Glu Pro Phe Gly Ile Ala Leu Ala Ile Cys Ala Ala  
1 5 10 15  
  
ctg ggt gtt gcc ttg acg ggc ttc gtg atg gcc gtc ttt atc aga ttc 95  
Leu Gly Val Ala Leu Thr Gly Phe Val Met Ala Val Phe Ile Arg Phe  
20 25 30  
  
cgc aac acc cca ata gtg aag gcc acg aac cga gaa ctg tcc tat gtc 143  
Arg Asn Thr Pro Ile Val Lys Ala Thr Asn Arg Glu Leu Ser Tyr Val  
35 40 45  
  
ctc ctg ttc tct ctc atc tgt tgc ttc tcc agt tcc ctc atc ttt att 191  
Leu Leu Phe Ser Leu Ile Cys Cys Phe Ser Ser Ser Leu Ile Phe Ile  
50 55 60  
  
gga gag ccg cag gat tgg atg tgt cgt tta cgc caa cct gcc ttt ggg 239  
Gly Glu Pro Gln Asp Trp Met Cys Arg Leu Arg Gln Pro Ala Phe Gly  
65 70 75  
  
atc agt ttt gtt ctc tgt atc tcc tgc atc ctt gtg aaa act aat aga 287  
Ile Ser Phe Val Leu Cys Ile Ser Cys Ile Leu Val Lys Thr Asn Arg  
80 85 90 95  
  
gta ctc tta gta ttt gaa gcc aag atc ccc aca agt ctc cat cgt aaa 335  
Val Leu Leu Val Phe Glu Ala Lys Ile Pro Thr Ser Leu His Arg Lys  
100 105 110  
  
tgg tgg ggg tta aac ctt cag ttt ttg ctg gtg ttt ctg tgc aca ttt 383  
Trp Trp Gly Leu Asn Leu Gln Phe Leu Leu Val Phe Leu Cys Thr Phe  
115 120 125  
  
gtc caa gtc atg atc tgt gtt gtc tgg ctg tac aat gcc cct ccc tcc 431  
Val Gln Val Met Ile Cys Val Val Trp Leu Tyr Asn Ala Pro Pro Ser  
130 135 140  
  
agt tac agg aat tat gac ata gat gag atg att ttt atc aca 473  
Ser Tyr Arg Asn Tyr Asp Ile Asp Glu Met Ile Phe Ile Thr  
145 150 155  
  
tg 475  
  
<210> 10  
<211> 157

100164961001  
"954949"

&lt;212&gt; PRT

&lt;213&gt; paralichthys dentatus

&lt;400&gt; 10

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Ser Trp Thr Glu Pro Phe Gly Ile Ala Leu Ala Ile Cys Ala Ala Leu
 1          5          10          15
Gly Val Ala Leu Thr Gly Phe Val Met Ala Val Phe Ile Arg Phe Arg
          20          25          30
Asn Thr Pro Ile Val Lys Ala Thr Asn Arg Glu Leu Ser Tyr Val Leu
          35          40          45
Leu Phe Ser Leu Ile Cys Cys Phe Ser Ser Ser Leu Ile Phe Ile Gly
          50          55          60
Glu Pro Gln Asp Trp Met Cys Arg Leu Arg Gln Pro Ala Phe Gly Ile
65          70          75          80
Ser Phe Val Leu Cys Ile Ser Cys Ile Leu Val Lys Thr Asn Arg Val
          85          90          95
Leu Leu Val Phe Glu Ala Lys Ile Pro Thr Ser Leu His Arg Lys Trp
          100          105          110
Trp Gly Leu Asn Leu Gln Phe Leu Leu Val Phe Leu Cys Thr Phe Val
          115          120          125
Gln Val Met Ile Cys Val Val Trp Leu Tyr Asn Ala Pro Pro Ser Ser
          130          135          140
Tyr Arg Asn Tyr Asp Ile Asp Glu Met Ile Phe Ile Thr
145          150          155

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&lt;210&gt; 11

&lt;211&gt; 1308

&lt;212&gt; DNA

&lt;213&gt; cyclopterus lumpus

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (2)...(1306)

&lt;400&gt; 11

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a cgc cca ggg att gaa aaa ttt gag aag gag atg gag gag cga gac atc 49
  Arg Pro Gly Ile Glu Lys Phe Glu Lys Glu Met Glu Glu Arg Asp Ile
   1          5          10          15

tgc att cac ctt aat gaa ctt atc tct cag tat ttt gag gag cat gaa 97
Cys Ile His Leu Asn Glu Leu Ile Ser Gln Tyr Phe Glu Asp His Glu
          20          25          30

atc caa gcg ctg gct gac agg att gag aac tcc aca gct aaa gtc atc 145
Ile Gln Ala Leu Ala Asp Arg Ile Glu Asn Ser Thr Ala Lys Val Ile
          35          40          45

gta gtg ttt gcc agc ggc cca gat atc gag cct tta atc aaa gag atg 193
Val Val Phe Ala Ser Gly Pro Asp Ile Glu Pro Leu Ile Lys Glu Met
          50          55          60

gtg agg aga aac atc aca gac cgt atc tgg tta gcc agt gaa gcg tgg 241
Val Arg Arg Asn Ile Thr Asp Arg Ile Trp Leu Ala Ser Glu Ala Trp
          65          70          75          80

gct agc tcc tct ctt ata gct aaa cca gag tat ctt gat gtt gtg gct 289
Ala Ser Ser Ser Leu Ile Ala Lys Pro Glu Tyr Leu Asp Val Val Ala
          85          90          95

```

ggg act atc ggc ttt gct ctc aag gca ggg cat att cct ggc tta aga	337
Gly Thr Ile Gly Phe Ala Leu Lys Ala Gly His Ile Pro Gly Leu Arg	
100 105 110	
gag ttc cta cag caa gtg caa cca aag aga gac agt cat aat gaa ttt	385
Glu Phe Leu Gln Gln Val Gln Pro Lys Arg Asp Ser His Asn Glu Phe	
115 120 125	
gtc agg gag ttt tgg gaa gaa acc ttc aac tgt tat ctg gaa gac agc	433
Val Arg Glu Phe Trp Glu Glu Thr Phe Asn Cys Tyr Leu Glu Asp Ser	
130 135 140	
cag aga cag cag gaa agt gag aat ggc agc aca agt ttc agg cct ttg	481
Gln Arg Gln Gln Glu Ser Glu Asn Gly Ser Thr Ser Phe Arg Pro Leu	
145 150 155 160	
tgt act ggt gag gaa gac atc aca agt gtt gag acc cag tac ttg gac	529
Cys Thr Gly Glu Glu Asp Ile Thr Ser Val Glu Thr Pro Tyr Leu Asp	
165 170 175	
tac aca cac ttt cgt atc tcc tat aac gtg tat gtt gca gtt tat tcc	577
Tyr Thr His Phe Arg Ile Ser Tyr Asn Val Tyr Val Ala Val Tyr Ser	
180 185 190	
att gca cag gcc ctg cag gac ata ctc acc tgc aca cct gga cat gga	625
Ile Ala Gln Ala Leu Gln Asp Ile Leu Thr Cys Thr Pro Gly His Gly	
195 200 205	
ctc ttt gcc aac aat tcc tgt gcc gat ata aag aaa atg gaa gca tgg	673
Leu Phe Ala Asn Asn Ser Cys Ala Asp Ile Lys Lys Met Glu Ala Trp	
210 215 220	
cag gcc ctg aag cag ctt aga cat ttg aac tac acc aac agc atg ggg	721
Gln Ala Leu Lys Gln Leu Arg His Leu Asn Tyr Thr Asn Ser Met Gly	
225 230 235 240	
gaa aag atg cac ttt gat gag aac tca gac atg gca tca aac tac acc	769
Glu Lys Met His Phe Asp Glu Asn Ser Asp Met Ala Ser Asn Tyr Thr	
245 250 255	
att ata aac tgg cac cgg tct gct gag gat ggc tct gtg gtg ttt gag	817
Ile Ile Asn Trp His Arg Ser Ala Glu Asp Gly Ser Val Val Phe Glu	
260 265 270	
gac gtg gga tac tac agc atg cac gtc aag aga gga gcc aaa ctg ttc	865
Asp Val Gly Tyr Tyr Ser Met His Val Lys Arg Gly Ala Lys Leu Phe	
275 280 285	
att gac aag aca aag att ttg tgg aat gga tac agt tgc gag gcg cca	913
Ile Asp Lys Thr Lys Ile Leu Trp Asn Gly Tyr Ser Ser Glu Ala Pro	
290 295 300	
ttc tct aat tgc agt gag gac tgt gaa cct ggt aca agg aag ggg atc	961
Phe Ser Asn Cys Ser Glu Asp Cys Glu Pro Gly Thr Arg Lys Gly Ile	
305 310 315 320	
att gac agt atg ccc aca tgt tgc ttt gaa tgc act gag tgc tca gat	1009
Ile Asp Ser Met Pro Thr Cys Cys Phe Glu Cys Thr Glu Cys Ser Asp	



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	325	330	335	
	gga gag tac agt aat cat aaa gat gcc agt gtt tgc acc aag tgt cca			1057
	Gly Glu Tyr Ser Asn His Lys Asp Ala Ser Val Cys Thr Lys Cys Pro			
	340	345	350	
	tat aac tct tgg tcc aat ggg aat cac aca ttc tgc ttc ctg aag gaa			1105
	Tyr Asn Ser Trp Ser Asn Gly Asn His Thr Phe Cys Phe Leu Lys Glu			
	355	360	365	
	atc gag ttt ctc tcc tgg aca gaa cca ttc ggg ata gct ttg gcc ata			1153
	Ile Glu Phe Leu Ser Trp Thr Glu Pro Phe Gly Ile Ala Leu Ala Ile			
	370	375	380	
	tgt gca gta ctg ggt gtg ctc ttg aca gct ttt gtg atc gga gtc ttt			1201
	Cys Ala Val Leu Gly Val Leu Leu Thr Ala Phe Val Ile Gly Val Phe			
	385	390	395	400
	gtc aga ttc cgc aac acc cca ata gtg aag gcc aca aac cga gaa ctg			1249
	Val Arg Phe Arg Asn Thr Pro Ile Val Lys Ala Thr Asn Arg Glu Leu			
	405	410	415	
	tcc tac gtt ctc ctg twc tca ctt atc tgt tgc ttc tca agc tcc ctc			1297
	Ser Tyr Val Leu Leu Xaa Ser Leu Ile Cys Cys Phe Ser Ser Ser Leu			
	420	425	430	
	akc ttc atc gg			1308
	Xaa Phe Ile			
	435			

<210> 12  
 <211> 435  
 <212> PRT  
 <213> cyclopterus lumpus  
 <220>  
 <221> VARIANT  
 <222> (1)...(435)  
 <223> Xaa = Any Amino Acid

<400> 12  
 Arg Pro Gly Ile Glu Lys Phe Glu Lys Glu Met Glu Glu Arg Asp Ile  
 1 5 10 15  
 Cys Ile His Leu Asn Glu Leu Ile Ser Gln Tyr Phe Glu Asp His Glu  
 20 25 30  
 Ile Gln Ala Leu Ala Asp Arg Ile Glu Asn Ser Thr Ala Lys Val Ile  
 35 40 45  
 Val Val Phe Ala Ser Gly Pro Asp Ile Glu Pro Leu Ile Lys Glu Met  
 50 55 60  
 Val Arg Arg Asn Ile Thr Asp Arg Ile Trp Leu Ala Ser Glu Ala Trp  
 65 70 75 80  
 Ala Ser Ser Ser Leu Ile Ala Lys Pro Glu Tyr Leu Asp Val Val Ala  
 85 90 95  
 Gly Thr Ile Gly Phe Ala Leu Lys Ala Gly His Ile Pro Gly Leu Arg  
 100 105 110  
 Glu Phe Leu Gln Gln Val Gln Pro Lys Arg Asp Ser His Asn Glu Phe  
 115 120 125  
 Val Arg Glu Phe Trp Glu Glu Thr Phe Asn Cys Tyr Leu Glu Asp Ser

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130 135 140  
 Gln Arg Gln Gln Glu Ser Glu Asn Gly Ser Thr Ser Phe Arg Pro Leu  
 145 150 155 160  
 Cys Thr Gly Glu Glu Asp Ile Thr Ser Val Glu Thr Pro Tyr Leu Asp  
 165 170 175  
 Tyr Thr His Phe Arg Ile Ser Tyr Asn Val Tyr Val Ala Val Tyr Ser  
 180 185 190  
 Ile Ala Gln Ala Leu Gln Asp Ile Leu Thr Cys Thr Pro Gly His Gly  
 195 200 205  
 Leu Phe Ala Asn Asn Ser Cys Ala Asp Ile Lys Lys Met Glu Ala Trp  
 210 215 220  
 Gln Ala Leu Lys Gln Leu Arg His Leu Asn Tyr Thr Asn Ser Met Gly  
 225 230 235 240  
 Glu Lys Met His Phe Asp Glu Asn Ser Asp Met Ala Ser Asn Tyr Thr  
 245 250 255  
 Ile Ile Asn Trp His Arg Ser Ala Glu Asp Gly Ser Val Val Phe Glu  
 260 265 270  
 Asp Val Gly Tyr Tyr Ser Met His Val Lys Arg Gly Ala Lys Leu Phe  
 275 280 285  
 Ile Asp Lys Thr Lys Ile Leu Trp Asn Gly Tyr Ser Ser Glu Ala Pro  
 290 295 300  
 Phe Ser Asn Cys Ser Glu Asp Cys Glu Pro Gly Thr Arg Lys Gly Ile  
 305 310 315 320  
 Ile Asp Ser Met Pro Thr Cys Cys Phe Glu Cys Thr Glu Cys Ser Asp  
 325 330 335  
 Gly Glu Tyr Ser Asn His Lys Asp Ala Ser Val Cys Thr Lys Cys Pro  
 340 345 350  
 Tyr Asn Ser Trp Ser Asn Gly Asn His Thr Phe Cys Phe Leu Lys Glu  
 355 360 365  
 Ile Glu Phe Leu Ser Trp Thr Glu Pro Phe Gly Ile Ala Leu Ala Ile  
 370 375 380  
 Cys Ala Val Leu Gly Val Leu Leu Thr Ala Phe Val Ile Gly Val Phe  
 385 390 395 400  
 Val Arg Phe Arg Asn Thr Pro Ile Val Lys Ala Thr Asn Arg Glu Leu  
 405 410 415  
 Ser Tyr Val Leu Leu Xaa Ser Leu Ile Cys Cys Phe Ser Ser Ser Leu  
 420 425 430  
 Xaa Phe Ile  
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<220>  
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<400> 13  
 Asp Asp Asp Tyr Gly Arg Pro Gly Ile Glu Lys Phe Arg Glu Glu Ala  
 1 5 10 15  
 Glu Glu Arg Asp Ile Cys Ile  
 20

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Ala	Arg	Ser	Arg	Asn	Ser	Ala	Asp	Gly	Arg	Ser	Gly	Asp	Asp	Leu	Pro
1				5				10						15	
Cys															

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24

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31